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1 CAAACTTGGT GGCAACTTGC CTCCCGGTGC GGGCGTCTCT CCCCCACCGT
51 CTCAA CATGC TTAGGGGTCC GGGGCCCCGGG CTGCTGCTGC TGGCCGTCCA
101 GTGCCTGGGG ACAGCGGTGC CCTCCACGGG AGCCTCGAAG AGCAAGAGGC
151 AGGCTCAGCA AATGGTTCAG CCCAGTCCC CGGTGGCTGT CAGTCAAAGC
201 AAGCCCGGTT GTTATGACAA TGGAAAACAC TATCAGATAA ATCAACAGTG
251 GGAGCGGACC TACCTAGGCA ATGCGTTGGT TTGTACTTGT TATGGAGGAA
301 GCCGAGGTTT TAACTGCGAG AGTAAACCTG AAGCTGAAGA GACTTGCTTT
351 GACAAGTACA CTGGGAACAC TTACCGAGTG GGTGACACTT ATGAGCGTCC
401 TAAAGACTCC ATGATCTGGG ACTGTACCTG CATCGGGGCT GGGCGAGGGA
451 GAATAAGCTG TACCATCGCA AACCGCTGCC ATGAAGGGGG TCAGTCCTAC
501 AAGATTGGTG ACACCTGGAG GAGACCACAT GAGACTGGTG GTTACATGTT
551 AGAGTGTGTG TGTCTTGGTA ATGGAAAAGG AGAATGGACC TGCAAGCCCA
601 TAGCTGAGAA GTGTTTTGAT CATGCTGCTG GGA CTTCCTA TGTGGTCGGA
651 GAAACGTGGG AGAAGCCCTA CCAAGGCTGG ATGATGGTAG ATTGTACTTG
701 CCTGGGAGAA GGCAGCGGAC GCATCACTTG CACTTCTAGA AATAGATGCA
751 ACGATCAGGA CACAAGGACA TCCTATAGAA TTGGAGACAC CTGGAGCAAG
801 AAGGATAATC GAGGAAACCT GCTCCAGTGC ATCTGCACAG GCAACGGCCG
851 AGGAGAGTGG AAGTGTGAGA GGCACACCTC TGTGCAGACC ACATCGAGCG
901 GATCTGGCCC CTTCACCGAT GTTCGTGCAG CTGTTTACCA ACCGCAGCCT
951 CACCCCCAGC CTCCTCCCTA TGGCCACTGT GTCACAGACA GTGGTGTGGT
1001 CTACTCTGTG GGGATGCAGT GGCTGAAGAC ACAAGGAAAT AAGCAAATGC
1051 TTTGCACGTG CCTGGGCAAC GGAGTCAGCT GCCAAGAGAC AGCTGTAACC

Fig 1 (part 1)

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1101 CAGACTTACG GTGGCAACTC AAATGGAGAG CCATGTGTCT TACCATTAC
1151 CTACAACGAC AGGACGGACA GCACAACTTC GAATTATGAG CAGGACCAGA
1201 AATACTCTTT CTGCACAGAC CACACTGTTT TGGTTCAGAC TCGAGGAGGA
1251 AATTCCAATG GTGCCTTGTG CCACTTCCCC TTCCTATACA ACAACCACAA
1301 TTACACTGAT TGCACTTCTG AGGGCAGAAG AGACAACATG AAGTGGTGTG
1351 GGACCACACA GAACTATGAT GCCGACCAGA AGTTTGGGTT CTGCCCCATG
1401 GCTGCCCACG AGGAAATCTG CACAACCAAT GAAGGGGTCA TGTACCGCAT
1451 TGGAGATCAG TGGGATAAGC AGCATGACAT GGGTCACATG ATGAGGTGCA
1501 CGTGTGTTGG GAATGGTCGT GGGGAATGGA CATGCATTGC CTACTCGCAG
1551 CTTGAGATC AGTGCATTGT TGATGACATC ACTTACAATG TGAACGACAC
1601 ATTCCACAAG CGTCATGAAG AGGGGCACAT GCTGAACTGT ACATGCTTCG
1651 GTCAGGGTCG GGGCAGGTGG AAGTGTGATC CCGTCGACCA ATGCCAGGAT
1701 TCAGAGACTG GGACGTTTTA TCAAATTGGA GATTCATGGG AGAAGTATGT
1751 GCATGGTGTC AGATACCACT GCTACTGCTA TGGCCGTGGC ATTGGGGAGT
1801 GGCATTGCCA ACCTTTACAG ACCTATCCAA GCTCAAGTGG TCCTGTCGAA
1851 GTATTTATCA CTGAGACTCC GAGTCAGCCC AACTCCCACC CCATCCAGTG
1901 GAATGCACCA CAGCCATCTC ACATTTCCAA GTACATTCTC AGGTGGAGAC
1951 CTGTGAGTAT CCCACCCAGA AACCTTGGAT ACTGAGTCTC CTAATCTTAT
2001 CAATTCTGAT GGTTTCTTTT TTTCCCAGCT TTTGAGCCAA CAACTCTGAT
2051 TAACTATTCC TATAGCATTT ACTATATTTG TTTAGTGAAC AAACAATATG
2101 TGGTCAATTA AATTGACTTG TAGACTGAAA AAAAAAAAAA AAAAAA

Fig 1 (part 2)

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	10	20	30	40	50	60
MSF-1 α	NLVATCLPVRASLPHRLN	MLRGP	GPGLLL	LAVQCLGTAVPSTGASKSKRQAQQMVPQSP		
fibronectin	NLVATCLPVRASLPHRLN	MLRGP	GPGLLL	LAVQCLGTAVPSTGASKSKRQAQQMVPQSP		
		10	20	30	40	
	70	80	90	100	110	120
MSF-1 α	VAVSQSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCE	SKPEAEETCFDKYT				
fibronectin	VAVSQSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCE	SKPEAEETCFDKYT				
	50	60	70	80	90	100
	130	140	150	160	170	180
MSF-1 α	GNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIGDTWRRPHETGG					
fibronectin	GNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANRCHEGGQSYKIGDTWRRPHETGG					
	110	120	130	140	150	160
	190	200	210	220	230	240
MSF-1 α	YMLECVCLGNGKGWETCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMVVDCTCLGEGSGR					
fibronectin	YMLECVCLGNGKGWETCKPIAEKCFDHAAGTSYVVGETWEKPYQGWMVVDCTCLGEGSGR					
	170	180	190	200	210	220
	250	260	270	280	290	300
MSF-1 α	ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNRGGEWK CERHTSVQTTSSG					
fibronectin	ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNRGGEWK CERHTSVQTTSSG					
	230	240	250	260	270	280
	310	320	330	340	350	360
MSF-1 α	SGPFTDVRAAVYQPQPHPQPPPYGHCVTDSGVVYSVGMQWLKTQGNKQMLCTCLGNGVSC					
fibronectin	SGPFTDVRAAVYQPQPHPQPPPYGHCVTDSGVVYSVGMQWLKTQGNKQMLCTCLGNGVSC					
	290	300	310	320	330	340
	370	380		390	400	
MSF-1 α	QETAVTQTYGGNSNGEPCVLPFTYNDRT-----DSTTSN	YEQDQKYSFCT				
fibronectin	QETAVTQTYGGNSNGEPCVLPFTYNGRTFYSC	TTEGRQDGHLCSTTSN	YEQDQKYSFCT			
	350	360	370	380	390	400
	410	420	430	440	450	460
MSF-1 α	DHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGR	RDNMKWC	GTTQNYDADQKFGFCP			
fibronectin	DHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGR	RDNMKWC	GTTQNYDADQKFGFCP			
	410	420	430	440	450	460

Fig. 2 (part 1)

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Binding site:

Sequence type:

5' untranslated
region

Signal

NH₂-terminal
segment

	Fibrin	Heparin	S. aureus
I			
I			
I			
I			
I			

Connecting strand

Gelatin

Unique sequence

3'untranslated
region

NLVA T C L P V R A S L P H R L N

MLRGGPGGLLLAVQCLGTAVPSTGASKSKR

PAGE TWO

"GIV BUN . . . GUX HMO IN QWIE R T Y . L GUN ALV . BUT GIV GUG SR GUF . FNU GUG SKPE ABET
 "GUF BUK YTGUN T GUR V GUGGUY E R P KDS . . MIMHD BUT GUGI GUA GUR GUR IS GUT IANR
 "GUG GEC . . . GUG GUGK I GUGGUG R P P H E T GUG YMLD BUT GUGI GUGN GUGK WT GUT IANR
 "GUG F D H A A G T GUGV V GUGGUG R P P Y . Q GUG MMLD BUT GUGI GUGI GUGS GUR IT GUT SRN
 "GUG BUN GUGDRT GUGUR I GUGGUGGUGS GUGDNR GUN . L LQ GUGI GUGI GUGI GUG MW GUR

U I T S V O T T S S G S G P F T D V R A A V Y Q P P P P P P P P P

$\text{C}^{\wedge}\text{GTV V N/S V GIM O HIL KGI}^{\wedge}\text{T Q GRN X Q M L GIT GHJL GYN GIH}^{\wedge}\text{V S GHQ E}$

1511 A V T R E Y E G I N S I N G E P C I V L R E A T X I N D R T - - - - - D S T I P S N I K E Q B U G H V S E I C T D H
1512 I V L O I R G E S I N G A L C S H F P F I K N N H N Y T D C T S E G R R D N M K W C G E R P N E D A C T I S F G G E N P M A A H E E I

"C T T N E - G V M K R I G D Q H D K Q H D - M E H M M R C T C V S N E R G I E C U T C T I A Y S Q L R D Q
 "C I C I V D - D I T Y N V N D I F H K R H E - E S H M L N C T E F S Q E R G R Y K C E D P V D Q
 "C Q D S E T G T F Y Q I G D S H E K I - Y V H G T V R Y Q C T C I Y C E I I S I E K H C Q Q P L Q T Y P S S

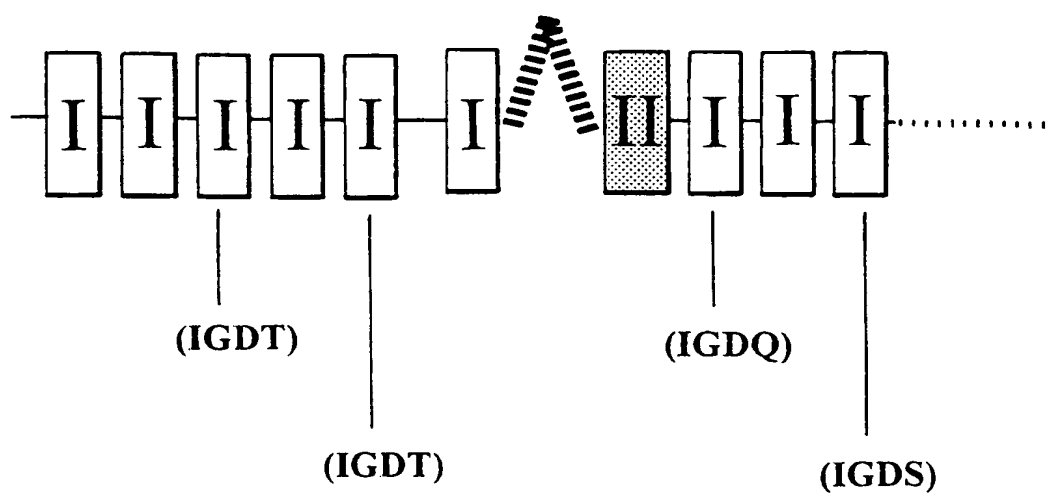
..S G P V E F I T E T P S Q P N S H P ^ I O P N A P I Q P S H T S K X I L R W R B

UW C I P P R N I. C Y642

VS*SYOE*WFLFFFPAFFPTTLINYSYSIYYICLVNKOYVVN*IDL*TEKKKKKK

Fig. 3

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*Fig. 4*

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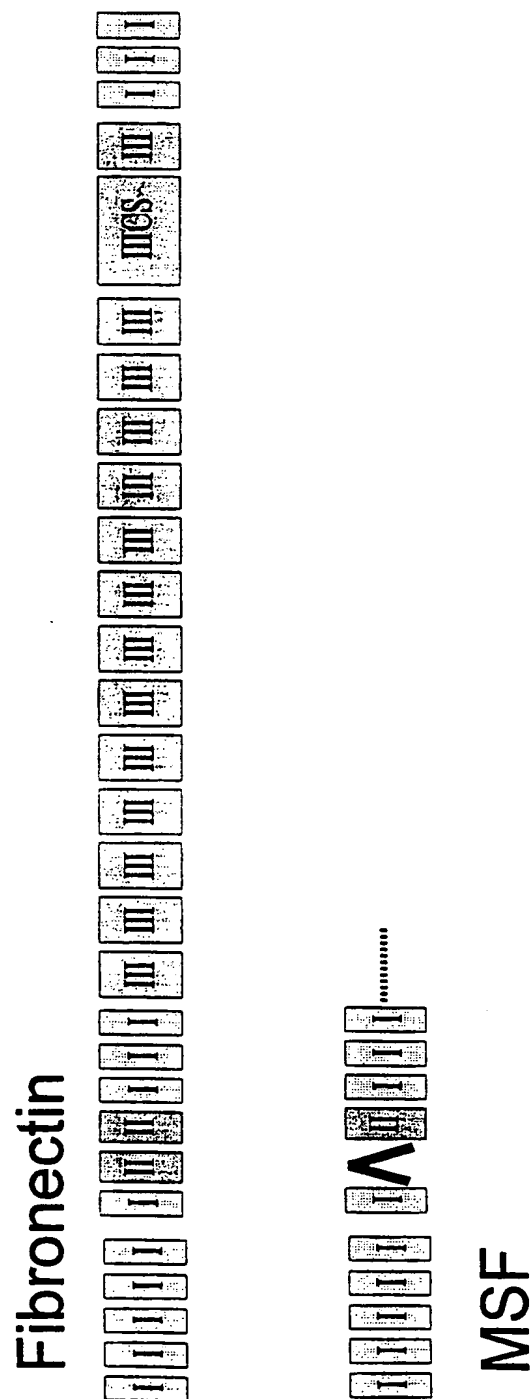


Fig. 5